

Alignments

>emb|V00866.1|HBVADW Hepatitis B virus complete DNA sequence (subtype adw)
Length=3200

Score = 5906 bits (3198), Expect = 0.0
Identities = 3198/3198 (100%), Gaps = 0/3198 (0%)
Strand=Plus/Plus

Query	3	TTCCACTGCCTTGCACCAAGCTCTGCAGGATCCCAGAGTCAGGGGTCTGTATCTTCCTGC	62
Sbjct	1	TTCCACTGCCTTGCACCAAGCTCTGCAGGATCCCAGAGTCAGGGGTCTGTATCTTCCTGC	60
Query	63	TGGTGGCTCCAGTTCAGGAACAGTAAACCCTGCTCCGAATATTGCCTCTCACATCTCGTC	122
Sbjct	61	TGGTGGCTCCAGTTCAGGAACAGTAAACCCTGCTCCGAATATTGCCTCTCACATCTCGTC	120
Query	123	AATCTCCGCGAGGACTGGGGACCCTGTGACGATCATGGAGAACATCACATCAGGATTCCCT	182
Sbjct	121	AATCTCCGCGAGGACTGGGGACCCTGTGACGATCATGGAGAACATCACATCAGGATTCCCT	180
Query	183	AGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACC	242
Sbjct	181	AGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACC	240
Query	243	GCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGATCACCCGTGTGTCT	302
Sbjct	241	GCAGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGATCACCCGTGTGTCT	300
Query	303	TGGCCAAAATTGCGAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTCCTCCAATTTG	362
Sbjct	301	TGGCCAAAATTGCGAGTCCCCAACCTCCAATCACTCACCAACCTCCTGTCCTCCAATTTG	360
Query	363	TCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCT	422
Sbjct	361	TCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCT	420
Query	423	ATGCCTCATCTTCTTATTGGTTCTTCTGGATTATCAAGGTATGTTGCCCGTTTGTCTCT	482
Sbjct	421	ATGCCTCATCTTCTTATTGGTTCTTCTGGATTATCAAGGTATGTTGCCCGTTTGTCTCT	480
Query	483	AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACCTGCACGACTCCTGCTCA	542
Sbjct	481	AATTCCAGGATCAACAACAACCAGTACGGGACCATGCAAAACCTGCACGACTCCTGCTCA	540
Query	543	AGGCAACTCTAAGTTTCCCTCATGTTGCTGTACAAAACCTACGGATGGAAATTGCACCTG	602
Sbjct	541	AGGCAACTCTAAGTTTCCCTCATGTTGCTGTACAAAACCTACGGATGGAAATTGCACCTG	600
Query	603	TATTCCCATCCCATCGTCTGGGCTTTTCGCAAAATACCTATGGGAGTGGGCCTCAGTCCG	662
Sbjct	601	TATTCCCATCCCATCGTCTGGGCTTTTCGCAAAATACCTATGGGAGTGGGCCTCAGTCCG	660
Query	663	TTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTTCAGTGGTTTCGTAGGGCTTTCCCCAC	722
Sbjct	661	TTTCTCTTGGCTCAGTTTACTAGTGCCATTTGTTTCAGTGGTTTCGTAGGGCTTTCCCCAC	720
Query	723	TGTTTGGCTTTTCAGCTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGT	782
Sbjct	721	TGTTTGGCTTTTCAGCTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGT	780
Query	783	GAGTCCCTTTTATACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACATTTAAACCT	842
Sbjct	781	GAGTCCCTTTTATACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACATTTAAACCT	840
Query	843	AACAAAACAAAAAGATGGGGTTATTCCCTAAACTTCATGGGCTACATAATTGGAAGTTGG	902
Sbjct	841	AACAAAACAAAAAGATGGGGTTATTCCCTAAACTTCATGGGCTACATAATTGGAAGTTGG	900
Query	903	GGAACTTTGCCACAGGATCATATTGTACAAAAGATCAAACACTGTTTTAGAAAACCTCCT	962
Sbjct	901	GGAACTTTGCCACAGGATCATATTGTACAAAAGATCAAACACTGTTTTAGAAAACCTCCT	960
Query	963	GTTAACAGGCCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGTCTTTTGGGCTTTGCT	1022
Sbjct	961	GTTAACAGGCCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGTCTTTTGGGCTTTGCT	1020
Query	1023	GCTCCATTTACACAATGTGGATATCCTGCCTTAATGCCTTTGTATGCATGTATACAAGCT	1082
Sbjct	1021	GCTCCATTTACACAATGTGGATATCCTGCCTTAATGCCTTTGTATGCATGTATACAAGCT	1080

Query	1083	AAACAGGCTTTTCACTTTCTCGCCAACCTTACAAGGCCTTTCTAAGTAAACAGTACATGAAC	1142
Sbjct	1081	AAACAGGCTTTTCACTTTCTCGCCAACCTTACAAGGCCTTTCTAAGTAAACAGTACATGAAC	1140
Query	1143	CTTTACCCCGTTTGCTCGGCAACGGCCTGGTCTGTGCCAAGTGTTTGCTGACGCAACCCCC	1202
Sbjct	1141	CTTTACCCCGTTTGCTCGGCAACGGCCTGGTCTGTGCCAAGTGTTTGCTGACGCAACCCCC	1200
Query	1203	ACTGGCTGGGGCTTAGCCATAGGCCATCAGCGCATGCGTGGAACCTTTGTGGCTCCTCTG	1262
Sbjct	1201	ACTGGCTGGGGCTTAGCCATAGGCCATCAGCGCATGCGTGGAACCTTTGTGGCTCCTCTG	1260
Query	1263	CCGATCCATACTGCGGAACCTCTAGCCGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAAG	1322
Sbjct	1261	CCGATCCATACTGCGGAACCTCTAGCCGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAAG	1320
Query	1323	CTCATCGGAACCTGACAATTCTGTCTGCTCTCTCGCGGAAATATACATCATTTCCATGGCTG	1382
Sbjct	1321	CTCATCGGAACCTGACAATTCTGTCTGCTCTCTCGCGGAAATATACATCATTTCCATGGCTG	1380
Query	1383	CTAGGCTGTACTGCCAACTGGATCCTTCGCGGGACGTCTTTGTTTACGTCCCGTCGGCG	1442
Sbjct	1381	CTAGGCTGTACTGCCAACTGGATCCTTCGCGGGACGTCTTTGTTTACGTCCCGTCGGCG	1440
Query	1443	CTGAATCCCGCGGACGACCCCTCTCGGGGCCGCTTGGGACTCTCTCGTCCCCTTCTCCGT	1502
Sbjct	1441	CTGAATCCCGCGGACGACCCCTCTCGGGGCCGCTTGGGACTCTCTCGTCCCCTTCTCCGT	1500
Query	1503	CTGCCGTTCCAGCCGACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGTCTGTGCCT	1562
Sbjct	1501	CTGCCGTTCCAGCCGACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGTCTGTGCCT	1560
Query	1563	TCTCATCTGCCGGTCCGTGTGCACTTCGCTTCACCTCTGCACGTTGCATGGCGACCACCG	1622
Sbjct	1561	TCTCATCTGCCGGTCCGTGTGCACTTCGCTTCACCTCTGCACGTTGCATGGCGACCACCG	1620
Query	1623	TGAACGCCCATCAGATCCTGCCAAAGGTCTTACATAAGAGGACTCTTGGAATCCCAGCAA	1682
Sbjct	1621	TGAACGCCCATCAGATCCTGCCAAAGGTCTTACATAAGAGGACTCTTGGAATCCCAGCAA	1680
Query	1683	TGTCAACGACCGACCTTGAGGCCTACTTCAAAGACTGTGTGTTTAAGGACTGGGAGGAGT	1742
Sbjct	1681	TGTCAACGACCGACCTTGAGGCCTACTTCAAAGACTGTGTGTTTAAGGACTGGGAGGAGT	1740
Query	1743	TGGGGGAGGAGATTAGGTAAATGATCTTTGTATTAGGAGGCTGTAGGCATAAATTGGTCT	1802
Sbjct	1741	TGGGGGAGGAGATTAGGTAAATGATCTTTGTATTAGGAGGCTGTAGGCATAAATTGGTCT	1800
Query	1803	GCGCACCAGCACCATGCAACTTTTTACCTCTGCCTAATCATCTCTTGTACATGTCCCAC	1862
Sbjct	1801	GCGCACCAGCACCATGCAACTTTTTACCTCTGCCTAATCATCTCTTGTACATGTCCCAC	1860
Query	1863	TGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCATGGACATTGACCCTTATAA	1922
Sbjct	1861	TGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCATGGACATTGACCCTTATAA	1920
Query	1923	AGAATTTGGAGCTACTGTGGAGTTACTCTCGTTTTTGCTTCTGACTTCTTTTCCTTCCGT	1982
Sbjct	1921	AGAATTTGGAGCTACTGTGGAGTTACTCTCGTTTTTGCTTCTGACTTCTTTTCCTTCCGT	1980
Query	1983	ACGAGATCTCCTAGACACCGCCTCAGCTCTGTATCGAGAAGCCTTAGAGTCTCCTGAGCA	2042
Sbjct	1981	ACGAGATCTCCTAGACACCGCCTCAGCTCTGTATCGAGAAGCCTTAGAGTCTCCTGAGCA	2040
Query	2043	TTGCTCACCTCACCATACTGCACTCAGGCAAGCCATTCTCTGCTGGGGGGAATTGATGAC	2102
Sbjct	2041	TTGCTCACCTCACCATACTGCACTCAGGCAAGCCATTCTCTGCTGGGGGGAATTGATGAC	2100
Query	2103	TCTAGCTACCTGGGTGGGTAATAATTTGCAAGATCCAGCATCCAGAGATCTAGTAGTCAA	2162
Sbjct	2101	TCTAGCTACCTGGGTGGGTAATAATTTGCAAGATCCAGCATCCAGAGATCTAGTAGTCAA	2160
Query	2163	TTATGTTAATACTAACATGGGTTTAAAGATCAGGCAACTATTGTGGTTTCATATATCTTG	2222
Sbjct	2161	TTATGTTAATACTAACATGGGTTTAAAGATCAGGCAACTATTGTGGTTTCATATATCTTG	2220
Query	2223	CCTTACTTTTGGGAAGAGAGACTGTACTTGAATATTTGGTCTCTTTTCGGAGTGTGGATTCTG	2282
Sbjct	2221	CCTTACTTTTGGGAAGAGAGACTGTACTTGAATATTTGGTCTCTTTTCGGAGTGTGGATTCTG	2280
Query	2283	CACTCCTCCAGCCTATAGACCACCAAATGCCCTATCTTATCAACACTTCCGGAAACTAC	2342

Sbjct	2281	CACTCCTCCAGCCTATAGACCACCAAATGCCCCCTATCTTATCAACACTTCCGGAAACTAC	2340
Query	2343	TGTTGTTAGACGACGGGACCGAGGCAGGTCCCCTAGAAGAAGAACTCCCTCGCCTCGCAG	2402
Sbjct	2341	TGTTGTTAGACGACGGGACCGAGGCAGGTCCCCTAGAAGAAGAACTCCCTCGCCTCGCAG	2400
Query	2403	ACGCAGATCTCAATCGCCGCGTCGCAGAAGATCTCAATCTCGGGAATCTCAATGTTAGTA	2462
Sbjct	2401	ACGCAGATCTCAATCGCCGCGTCGCAGAAGATCTCAATCTCGGGAATCTCAATGTTAGTA	2460
Query	2463	TTCTTGGACTCATAAGGTCGGAAACTTTACGGGGCTTTATTCTCTACAGTACCTATCT	2522
Sbjct	2461	TTCTTGGACTCATAAGGTCGGAAACTTTACGGGGCTTTATTCTCTACAGTACCTATCT	2520
Query	2523	TTAATCCTGAATGGCAAACCTCTTCTTTCTAAGATTCAATTTACAAGAGGACATTATTA	2582
Sbjct	2521	TTAATCCTGAATGGCAAACCTCTTCTTTCTAAGATTCAATTTACAAGAGGACATTATTA	2580
Query	2583	ATAGGTGTCAACAATTTGTGGGCCCTCTCACTGTAAATGAAAAGAGAAGATTGAAATTAA	2642
Sbjct	2581	ATAGGTGTCAACAATTTGTGGGCCCTCTCACTGTAAATGAAAAGAGAAGATTGAAATTAA	2640
Query	2643	TTATGCCTGCTAGATTCTATCCTACCCACACTAAATATTTGCCCTTAGACAAAGGAATTA	2702
Sbjct	2641	TTATGCCTGCTAGATTCTATCCTACCCACACTAAATATTTGCCCTTAGACAAAGGAATTA	2700
Query	2703	AACCTTATTATCCAGATCAGGTAGTTAATCACTTCCAAACCAGACATTATTTACATA	2762
Sbjct	2701	AACCTTATTATCCAGATCAGGTAGTTAATCACTTCCAAACCAGACATTATTTACATA	2760
Query	2763	CTCTTTGGAAGGCTGGTATTCTATATAAGAGGGAAACCACACGTAGCGCATCATTTTGCG	2822
Sbjct	2761	CTCTTTGGAAGGCTGGTATTCTATATAAGAGGGAAACCACACGTAGCGCATCATTTTGCG	2820
Query	2823	GGTCACCATATTCTTGGAACAAGAGCTACAGCATTGCAAAGGCATGGGGACGAATCTT	2882
Sbjct	2821	GGTCACCATATTCTTGGAACAAGAGCTACAGCATTGCAAAGGCATGGGGACGAATCTT	2880
Query	2883	TCTGTTCCCAACCCTCTGGGATTCTTCCCGATCATCAGTTGGACCCTGCATTTCGGAGCC	2942
Sbjct	2881	TCTGTTCCCAACCCTCTGGGATTCTTCCCGATCATCAGTTGGACCCTGCATTTCGGAGCC	2940
Query	2943	AACTCAACAAATCCAGATTGGGACTTCAACCCCATCAAGGACCACTGGCCAGCAGCCAAC	3002
Sbjct	2941	AACTCAACAAATCCAGATTGGGACTTCAACCCCATCAAGGACCACTGGCCAGCAGCCAAC	3000
Query	3003	CAGGTAGGAGTGGGAGCATTGGGGCCAGGGCTCACCCCTCCACACGGCGGTATTTTGGGG	3062
Sbjct	3001	CAGGTAGGAGTGGGAGCATTGGGGCCAGGGCTCACCCCTCCACACGGCGGTATTTTGGGG	3060
Query	3063	TGGAGCCCTCAGGCTCAGGGCATATTGACCACAGTGTCAACAATTCCTCCTCCTGCCTCC	3122
Sbjct	3061	TGGAGCCCTCAGGCTCAGGGCATATTGACCACAGTGTCAACAATTCCTCCTCCTGCCTCC	3120
Query	3123	ACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCTCCACCTCTAAGAGACAGTCAT	3182
Sbjct	3121	ACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCTCCACCTCTAAGAGACAGTCAT	3180
Query	3183	CCTCAGGCCATGCAGTGG	3200
Sbjct	3181	CCTCAGGCCATGCAGTGG	3198